

SEQUENCE LISTING

(1) GENERAL INFORMATION:

- (i) APPLICANT: Cerretti, Douglas P.
- (ii) TITLE OF INVENTION: Cytokine Designated as LERK-6
- (iii) NUMBER OF SEQUENCES: 8
- (iv) CORRESPONDENCE ADDRESS:
 - (A) ADDRESSEE: Immunex Corporation
 - (B) STREET: 51 University Street
 - (C) CITY: Seattle
 - (D) STATE: WA
 - (E) COUNTRY: USA
 - (F) ZIP: 98101
- (v) COMPUTER READABLE FORM:
 - (A) MEDIUM TYPE: Floppy disk
 - (B) COMPUTER: Apple Macintosh
 - (C) OPERATING SYSTEM: System 7.1
 - (D) SOFTWARE: PatentIn Release #1.0, Version #1.25
- (vi) CURRENT APPLICATION DATA:
 - (A) APPLICATION NUMBER: US --to be assigned--
 - (B) FILING DATE:
 - (C) CLASSIFICATION:
- (viii) ATTORNEY/AGENT INFORMATION:
 - (A) NAME: Malaska, Stephen L.
 - (B) REGISTRATION NUMBER: 32,655
 - (C) REFERENCE/DOCKET NUMBER: 2826
- (ix) TELECOMMUNICATION INFORMATION:
 - (A) TELEPHONE: (206) 587-0430
 - (B) TELEFAX: (206) 233-0644

(2) INFORMATION FOR SEQ ID NO:1:

- (i) SEQUENCE CHARACTERISTICS:
 - (A) LENGTH: 555 base pairs
 - (B) TYPE: nucleic acid
 - (C) STRANDEDNESS: single
 - (D) TOPOLOGY: linear
- (ii) MOLECULE TYPE: cDNA
- (iii) HYPOTHETICAL: NO
- (iv) ANTI-SENSE: NO
- (vii) IMMEDIATE SOURCE:
 - (B) CLONE: LERK-6
- (ix) FEATURE:
 - (A) NAME/KEY: CDS

(B) LOCATION: 1..552

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:1:

GCC CGG GCC AAC GCT GAC CGA TAC GCA GTC TAC TGG AAC CGT AGC AAC	48
Ala Arg Ala Asn Ala Asp Arg Tyr Ala Val Tyr Trp Asn Arg Ser Asn	
1 5 10 15	
CCC AGG TTT CAG GTG AGC GCT GTG GGT GAT GGC GGC GGC TAT ACC GTG	96
Pro Arg Phe Gln Val Ser Ala Val Gly Asp Gly Gly Gly Tyr Thr Val	
20 25 30	
GAG GTG AGC ATC AAC GAC TAC CTG GAT ATC TAC TGC CCA CAC TAC GGG	144
Glu Val Ser Ile Asn Asp Tyr Leu Asp Ile Tyr Cys Pro His Tyr Gly	
35 40 45	
GCG CCG CTG CCC CCG GCT GAG CGC ATG GAG CGG TAC ATC CTG TAC ATG	192
Ala Pro Leu Pro Pro Ala Glu Arg Met Glu Arg Tyr Ile Leu Tyr Met	
50 55 60	
GTG AAT GGT GAG GGC CAC GCC TCC TGT GAC CAC CGG CAG CGA GGC TTC	240
Val Asn Gly Glu Gly His Ala Ser Cys Asp His Arg Gln Arg Gly Phe	
65 70 75 80	
AAG CGC TGG GAA TGC AAC CGG CCC GCA GCG CCC GGG GGA CCC CTC AAG	288
Lys Arg Trp Glu Cys Asn Arg Pro Ala Ala Pro Gly Gly Pro Leu Lys	
85 90 95	
TTC TCA GAG AAG TTC CAA CTC TTC ACC GCG TAT TTC CTG GGC TTT GAG	336
Phe Ser Glu Lys Phe Gln Leu Phe Thr Pro Phe Ser Leu Gly Phe Glu	
100 105 110	
TTC CGG CCT GGC CAC GAA TAC TAC TAC ATC TCT GGC ACA CCT CCC AAC	384
Phe Arg Pro Gly His Glu Tyr Tyr Tyr Ile Ser Ala Thr Pro Pro Asn	
115 120 125	
CTC GTG GAC CGA CCC TGC CTG CGA CTC AAG GTT TAT GTG CGT CCA AAC	432
Leu Val Asp Arg Pro Cys Leu Arg Leu Lys Val Tyr Val Arg Pro Thr	
130 135 140	
AAT GAG ACC CTG TAT GAG GGT GCA GAG CCC ATC TTC ACC AGT AAC AGC	480
Asn Glu Thr Leu Tyr Glu Ala Pro Glu Pro Ile Phe Thr Ser Asn Ser	
145 150 155 160	
TCC TGC AGC GGC CTG GGT GGC TGC CAC CTC TTC CTC ACC ACC GTC GGT	528
Ser Cys Ser Gly Leu Gly Gly Cys His Leu Phe Leu Thr Thr Val Pro	
165 170 175	
GTG CTG TGG TCC CTT CTG GGC TCC TAC	555
Val Leu Trp Ser Leu Leu Gly Ser	
180	

(2) INFORMATION FOR SEQ ID NO:2:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 184 amino acids
 (B) TYPE: amino acid

(D) TOPOLOGY: linear

(ii) MOLECULE TYPE: protein

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:2:

Ala Arg Ala Asn Ala Asp Arg Tyr Ala Val Tyr Trp Asn Arg Ser Asn
 1 5 10 15
 Pro Arg Phe Gln Val Ser Ala Val Gly Asp Gly Gly Gly Tyr Thr Val
 20 25 30
 Glu Val Ser Ile Asn Asp Tyr Leu Asp Ile Tyr Cys Pro His Tyr Gly
 35 40 45
 Ala Pro Leu Pro Pro Ala Glu Arg Met Glu Arg Tyr Ile Leu Tyr Met
 50 55 60
 Val Asn Gly Glu Gly His Ala Ser Cys Asp His Arg Gln Arg Gly Phe
 65 70 75 80
 Lys Arg Trp Glu Cys Asn Arg Pro Ala Ala Pro Gly Gly Pro Leu Lys
 85 90 95
 Phe Ser Glu Lys Phe Gln Leu Phe Thr Pro Phe Ser Leu Gly Phe Glu
 100 105 110
 Phe Arg Pro Gly His Glu Tyr Tyr Tyr Ile Ser Ala Thr Pro Pro Asn
 115 120 125
 Leu Val Asp Arg Pro Cys Leu Arg Leu Lys Val Tyr Val Arg Pro Thr
 130 135 140
 Asn Glu Thr Leu Tyr Glu Ala Pro Glu Pro Ile Phe Thr Ser Asn Ser
 145 150 155 160
 Ser Cys Ser Gly Leu Gly Gly Cys His Leu Phe Leu Thr Thr Val Pro
 165 170 175
 Val Leu Trp Ser Leu Leu Gly Ser
 180

(2) INFORMATION FOR SEQ ID NO:3:

- (i) SEQUENCE CHARACTERISTICS:
 (A) LENGTH: 28 base pairs
 (B) TYPE: nucleic acid
 (C) STRANDEDNESS: single
 (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: RNA

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:3:

GATATTTACT GCCCGCACTA CAACAGCT

(2) INFORMATION FOR SEQ ID NO:4:

- (i) SEQUENCE CHARACTERISTICS:
 - (A) LENGTH: 25 base pairs
 - (B) TYPE: nucleic acid
 - (C) STRANDEDNESS: single
 - (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: cDNA

(iii) HYPOTHETICAL: NO

(iv) ANTI-SENSE: NO

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:4:

AGAGAAGGCG CTGTAGCGCT GGAAC

25

(2) INFORMATION FOR SEQ ID NO:5:

- (i) SEQUENCE CHARACTERISTICS:
 - (A) LENGTH: 31 base pairs
 - (B) TYPE: nucleic acid
 - (C) STRANDEDNESS: single
 - (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: cDNA

(iii) HYPOTHETICAL: NO

(iv) ANTI-SENSE: NO

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:5:

ACGTAGTCTA CTGGAAGTCC AGTAACCCCA G

31

(2) INFORMATION FOR SEQ ID NO:6:

- (i) SEQUENCE CHARACTERISTICS:
 - (A) LENGTH: 34 base pairs
 - (B) TYPE: nucleic acid
 - (C) STRANDEDNESS: single
 - (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: cDNA

(iii) HYPOTHETICAL: NO

(iv) ANTI-SENSE: NO

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:6:

AGCCTCAAGC ACTGGCCAGA ACTCTCTCTG GAGT

34

(2) INFORMATION FOR SEQ ID NO:7:

- (i) SEQUENCE CHARACTERISTICS:
 (A) LENGTH: 314 base pairs
 (B) TYPE: nucleic acid
 (C) STRANDEDNESS: single
 (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: cDNA to mRNA

(iii) HYPOTHETICAL: NO

(iv) ANTI-SENSE: NO

(ix) FEATURE:

- (A) NAME/KEY: CDS
 (B) LOCATION: 2..313

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:7:

G TTC CAC GCA GGC GCG GGG GAC GAC GGC GGG GGC TAC ACG GTG GAG	46
Phe His Ala Gly Ala Gly Asp Asp Gly Gly Gly Tyr Thr Val Glu	15
1 5 10	
GTG AGC ATC AAT GAC TAC CTG GAC ATC TAC TGC CCG CAC TAT GGG GCG	94
Val Ser Ile Asn Asp Tyr Leu Asp Ile Tyr Cys Pro His Tyr Gly Ala	30
20 25 30	
CCG CTG CCG CCG GCC GAG CGC ATG GAG CAC TAC GTG CTG TAC ATG GTC	142
Pro Leu Pro Pro Ala Glu Arg Met Glu His Tyr Val Leu Tyr Met Val	45
35 40 45	
AAC GGC GAG GGC CAC GCC TCC TGC GAC CAC CGC CAG CGC GGC TTC AAG	190
Asn Gly Glu Gly His Ala Ser Cys Asp His Arg Gln Arg Gly Phe Lys	60
50 55 60	
CGC TGG GAG TGC AAC CCG CCC GCG GCG CCC GGG GGG CCG CTC AAG TTC	238
Arg Trp Glu Cys Asn Arg Pro Ala Ala Pro Gly Gly Pro Leu Lys Phe	75
65 70 75	
TCG GAG AAG TTC CAG CTC TTC ACG CCC TTC TCC CTG GGC TTC GAG TTC	286
Ser Glu Lys Phe Gln Leu Phe Thr Pro Phe Ser Leu Gly Phe Glu Phe	95
80 85 90 95	
CGG CCC GGC CAC GAG TAT TAC TAC ATC T	314
Arg Pro Gly His Glu Tyr Tyr Tyr Ile	100
100	

(2) INFORMATION FOR SEQ ID NO:8:

- (i) SEQUENCE CHARACTERISTICS:
 (A) LENGTH: 104 amino acids
 (B) TYPE: amino acid
 (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: protein

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:8:

Phe His Ala Gly Ala Gly Asp Asp Gly Gly Gly Tyr Thr Val Glu Val
1 5 10 15
Ser Ile Asn Asp Tyr Leu Asp Ile Tyr Cys Pro His Tyr Gly Ala Pro
20 25 30
Leu Pro Pro Ala Glu Arg Met Glu His Tyr Val Leu Tyr Met Val Asn
35 40 45
Gly Glu Gly His Ala Ser Cys Asp His Arg Gln Arg Gly Phe Lys Arg
50 55 60
Trp Glu Cys Asn Arg Pro Ala Ala Pro Gly Gly Pro Leu Lys Phe Ser
65 70 75 80
Glu Lys Phe Gln Leu Phe Thr Pro Phe Ser Leu Gly Phe Glu Phe Arg
85 90 95
Pro Gly His Glu Tyr Tyr Tyr Ile
100